

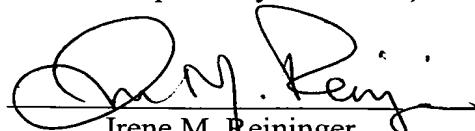
REMARKS

Applicant made an inadvertent error in SEQ ID NO: 1 in the specification (see page 40 of the pending U.S. Provisional Patent Application No. 60/458,946 to which this application claims priority). SEQ ID NO:1 is a full-length amino acid sequence of a wild-type human PDE1B. This sequence was published prior to the filing date of the pending provisional referred to above, e.g., see *Cell. Signal.* 9:519-526, specifically, page 522 (1997) (attached for the Examiner's convenience). This paper is described in the specification of the pending provisional noted above, together with the specification of the application being filed concurrent herewith, e.g., see page 3, line 13 (pending provisional) and page 3, line 17 (application being filed concurrent herewith). Applicant inadvertently listed the first 60 amino acids at the end of the sequence versus in their rightful place at the beginning, as amino acids 1-60. Applicant is filing this preliminary amendment to merely correct the positioning of the first 60 amino acids. As the Examiner will fully appreciate, no new matter is being added by this amendment, given that Applicant had described the above article in the specification of the pending provisional to which the application being filed concurrent herewith claims priority. Pending entry of the amendment, SEQ ID NO:1, once again, a sequence in the public domain prior to the filing date of the pending provisional to which the application being filed concurrent herewith claims priority will now correctly reflect the sequence published in the above noted article.

Applicant regrets any inconvenience to the Examiner due to Applicant's inadvertent error, and respectfully requests entry of the amendment hereinabove, and an early examination and allowance of the claims.

Respectfully submitted,

Date: 3/31/04



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	GCA GCG GGA GAG GAG GAG CCG CAG GAG CTG CAG CTC TGC CAG CTT GGG CCG AGC CTA GAG ACA CCG GCC TGG CTG	75
	GTC CAC GCC AGC CCG AGA CCG TGG CTG AGC ATG GAG CTG TCA CCC CCG AGT CCT CCG GAG ATG CTG GAG GAG TCG	150
	M E L S P R S P P E M L E E S	
16	GAT TGC CCG TCA CCC CTG GAG CTG AAG TCA GCC CCC AGC AAG AAG ATG TGG ATT AAG CTT CGG TCT CTG CTG CGC	225
	D C P S P L E L K S A P S K K M W I K L R S L L R	
41	TAC ATG GTG AAG CAG CAG TTG GAG AAT GGG GAG ATA AAC ATT GAG GAG CTG AAG AAA AAT CTG GAG TAC ACA GCT TCT	300
	Y M V K Q L E N G E I N I E E L K K N L E Y T A S	
66	CTG CTG GAA GCC GTC TAC ATA GAT GAG ACA CGG CAA ATC TTG GAC ACC GAG GAC GAG CTG CAG GAG CTG CGG TCA	375
	L L E A V Y I D E T R Q I L D T E D E L Q E L R S	
91	GAT GCC GTG CCT TCG GAG GTG CGG GAC TGG CTG GCC TCC ACC TTC ACC CAG CAG GCC CGG GCC AAA GGC CGC CGA	450
	D A V P S E V R D W L A S T F T Q Q A R A K G R R	
116	GCA GAG GAG AAG CCC AAG TTC CGA AGC ATT GTG CAC GCT GTG CAG GCT GGG ATC TTC GTG GAA CGG ATG TTC CGG	525
	A E E K P K F R S I V H A V Q A G I P V E R M F R	
141	AGA ACA TAC ACC TCT GTG GGC CCC ACT TAC TCT ACT GCG GTT CTC AAC TGT CTC AAC AAC CTG GAT CTC TGG TGC	600
	R T Y T S V G P T Y S T A V L N C L K N L D L W C	
166	TTT GAT GTC TTT TCC TTG AAC CAG GCA GCA GAT GAC CAT GCC CTG AGG ACC ATT GTT TTT GAG TTG CTG ACT CGG	675
	Y D V F S L N Q A A D D H A L R T I V F E L L T R	
191	CAT AAC CTC ATC AGC CGC TTC AAG ATT CCC ACT GTG TTT TTG ATG AGT TTC CTG GAT GCC TTG GAG ACA GGC TAT	750
	H H L I S R F R I P T V F L M S F L D A L E T G Y	
216	GGG AAG TAC AAG AAT CCT TAC CAC AAC CAG ATC CAC GCA GCC GAT GTT ACC CAG ACA GTC CAT TGC TTC TTG CTC	825
	G K Y K N P Y H N Q I H A A D V T Q T V H C F L L	
241	CGC ACA GGG ATG GTG CAC TGC CTG TCG GAG ATT GAG CTC CTG GCC ATC ATC TTT GCT GCA GCT ATC CAT GAT TAT	900
	R T G M V H C L S E I E L L A X X F A A A I H D Y	
266	GAG CAC ACC GGC ACT ACC AAC AGC TTC CAC ATC CAG ACC AAG TCA GAA TGT GCC ATC GTG TAC AAT GAT CGT TCA	975
	E H T G T T N S F H I Q T K S E C A I V Y N D R S	
291	GTG CTG GAG AAT CAC CAC ATC AGC TCT GTT TTC CGA TTG ATG CAG GAT GAT GAG ATG AAC ATT TTC ATC AAC CTC	1050
	V L E N H H I S S V F R L M Q D D E M N I F I N L	
316	ACC AAG GAT GAG TTT GTA GAA CTC CGA GCC CTG GTC ATT GAG ATG GTG TTG GCC ACA GAC ATG TCC TGC CAT TTC	1125
	T K D E F V E L R A L V I E M V L A T D M S C H F	
341	CAG CAA GTG AAG ACC ATG AAG ACA GCC TTG CAA CAG CTG GAG AGG ATT GAC AAG CCC AAG GCC CTG TCT CTA CTG	1200
	Q Q V K T M K T A L Q Q L E R I D K P K A L S L L	
366	CTC CAT GCT GCT GAC ATC AGC CAC CCA ACC AAG CAG TGG TTG GTC CAC AGC CGT TGG ACC AAG GCC CTC ATG GAG	1275
	L H A A D I S H P T K Q W L V H S R W T K A L M E	
391	GAA TTC TTC CGT CAG GGT GAC AAG GAG GCA GAG TTG GGC CTG CCC TTT TCT CCA CTC TGT GAC CGC ACT TCC ACT	1350
	E F F R Q G D K E A E L G L F P S P L C D R T S T	
416	CTA GTG GCA CAG TCT CAG ATA GGG TTC ATC GAC TTC ATT GTG GAG CCC ACA TTC TCT GTG CTG ACT GAC GTG GCA	1425
	L V A Q S Q I G F I D F I V E P T F S V L T D V A	
441	GAG AAG AGT GTT CAG CCC CTG GCG GAT GAG GAC TCC AAG TCT AAA AAC CAG CCC AGC TTT CAG TGG CGC CAG CCC	1500
	E K S V Q P L A D E D S K S K N Q P B F Q W R Q P	
466	TCT CTG GAT GTG GAA GTG GGA GAC CCC AAC CCT GAT GTG GTC AGC TTT CGT TCC ACC TCG GTC AAG CCC ATT CAG	1575
	S L D V E V G D P N P D D V W S F R S T W V K R I Q	
491	GAG AAC AAG CAG AAA TGG AAG GAA CGG GCA GCA AGT GGC ATC ACC AAC CAG ATG TCC ATT GAC GAG CTG TCC CCC	1650
	E N K Q K W K E R A A S G I T N Q M S I D E L S P	
516	TGT GAA GAA GAG GCC CCC CCA TCC CCT GCC GAA GAT GAA CAC AAC CAG AAT GGG ATT CTG GAT TAG CCC TGG GGC	1725
	C E E E A P P S F A E D E H N Q H G N L D	
	TGG CCC AGG TCT TCA TTG AGT CCA AAG TGT TTG ATG TCA TCA GCA CCA TCC ATC AGG ACT GGC TCC CCC ATC TGC	1800
	TCC AAG GGA GCG TGG TCG TGG AAG AAA CAA CCC ACC TGA AGG CCA ATT GGC AGA GAT TTG GGG TTG GGG AAA GGG	1875
	CCC CTC CCC ACC TGA CAC CCA CTG GGG TGC ACT TTA ATG TTC CGG CAG CAA GAC TGG GGA ACT TCA GGC TCC CAG	1950
	TGG TCA CTG TGC CCA TCC CTC AGC CTC TGG ATT CTC TTC ATG GCC AGG TGG CTG CCA GGG AGC GGG GAG CTT CCT	2025
	GGA GGC TTC CCA GGG CCT TGG GGA AGG GTC AGA GAT GCC AGC CCC CTG GGA CCT CCC CCA TCC TTT TTG CCT CCA	2100
	AGT TTC TAA GCA ATA CAT TTT GGG GGT TCC CTC AGC CCC CCA CCC CAG ATC TTA GCT GGC AGG TCT GGG TGC CCC	2175
	TTT TCC TCC CCT GGG AAG GGC TGG ATT AGG ATA GAA AGC TGG GGG TTT TCA GAG CCC ATT GTG TGG GGA GGG GAG	2250
	TGG ATT CCT TCA GGG CAT GGT ACC TTT CTA GGA CCT GGG AAT GGG GTG GAG AGG ACG TCC TCT TCA CCC CAG AAT	2325
	TGC GCT GCT TCA GCC CCA CCT CCA CCC TGA TCC TCT GAA CCT TCC TCC CCT CCA TTT CTG ATA TAG TGA CTG GGG	2400
	CAA AAG GAG CCA TTG TGA CCA GGG GCT GCG GGA GGC CCT TCC TGG GAC CCT TGG TCT GGG CCC TGG	2475
	GGT TTG TCG CCT GCC CTG AGT CCG GAG CCC TTT GCC TCC TTC CTC TCC CCT GGG CCT GGG AGG CTC CAT CCG ACC	2550
	AAT GTC TGT AAA GTG CTT TGA GGA TCT CCC CAG CAA AGC ACC TTC AGA ATG TAT CGA CAC CAG CTG GGT TAG GGT	2625
	CAA GGG TGC CTG GGG AGG G	2644

FIGURE 1. Nucleotide and predicted protein sequence of HSPDE1B1 cDNA. The cDNA sequence shown was constructed from overlapping sequences of clones FB56a (nucleotides 1–698) and FB29a (nucleotides 285–2644) isolated from a human foetal brain cDNA library. Nucleotide residues are numbered on the right. The predicted amino acid sequence is represented by single letter amino acid code beneath the nucleotide sequence and is numbered on the left.

of approximately 750 bp is obtained due to the presence of intronic sequences between the primers. No product of the expected size is obtained when either mouse or hamster genomic DNA is used as template.

PCR (12.5  $\mu$ l) was carried out with 0.1 U Taq Polymerase, 0.2 mM dNTPs, and 10  $\mu$ g/ml of each primer in standard reaction buffer (Boehringer Mannheim). Somatic cell hybrid DNA (0.25  $\mu$ l, representing 61–93 ng) was added as